

AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions and listings of claims in the application.

LISTING OF CLAIMS

1. (Currently amended) A method for classifying a patient having diffuse large B-cell lymphoma (DLBCL), the method comprising:

providing a plurality of primers designed to hybridize to a first plurality of genes in a tumor sample from the patient;

amplifying said first plurality of genes using said plurality of primers;

measuring expression of [[a]] said first plurality of genes[[,]] ~~in a tumor sample from the patient~~ to produce measured expression values;

normalizing said measured expression values of said plurality of genes to produce normalized expression values; [[and]]

correlating said normalized ~~tumor~~ expression values of said first plurality of genes to normalized reference expression values obtained for [[the]] a second plurality of genes from DLBCL patients stratified into said classification groups; and

classifying the patient into at least one of said classification groups.

2. (Currently amended) The method of claim 1, ~~wherein the method predicts patient~~
further comprising:

predicting survival of the patient wherein ~~[[the]]~~ said first and said second
plurality of genes comprise~~[[s]]~~ a plurality of genes predictive of survival probability and
wherein said classification groups comprise groups of said DLBCL patients having known
overall survival probability.

3. (Currently amended) The method of claim 2, wherein said known overall
survival probability comprises overall survival probability after anthracycline-based
chemotherapy.

4. (Currently amended) The method of claim 1, wherein said measuring expression
of said first plurality of genes in said tumor sample from the patient comprises performing
Real-Time RT-PCR on the tumor sample from the patient.

5. (Currently amended) The method of claim 1, wherein said normalized ~~tumor~~
expression values of said first plurality of genes ~~and normalized reference expression values~~
comprise ratios of measured expression values obtained from said first plurality of genes to
expression values of a housekeeping gene.

6. (Original) The method of claim 5, wherein the housekeeping gene is *PGK1* or
GAPDH.

7. (Original) The method of claim 6, wherein the housekeeping gene is *PGK1*.
8. (Currently amended) The method of claim 1, wherein ~~[[the]]~~ said normalized ~~tumor~~ expression values of said first plurality of genes ~~and normalized reference expression values~~ comprise ratios of measured expression values obtained from said first plurality of genes in said tumor ~~DLBCL cells~~ to measured expression values obtained from said first plurality of genes in a reference cell line.
9. (Original) The method of claim 8, wherein the reference cell line is a Raji cell line.
10. (Currently amended) The method of claim 1, ~~wherein expression values from DLBCL patients have been stratified based upon expression values for the plurality of genes by~~ further comprising:
performing univariate Cox proportional hazards analysis to stratify said normalized reference expression values with ~~[[the]]~~ said classification groups held as a dependent variable.

11. (Currently amended) The method of claim 2, ~~wherein expression values from DLBCL patients have been stratified base upon expression values for the plurality of genes by~~ further comprising:

performing univariate Cox proportional hazards analysis to stratify said normalized reference expression values with said known overall survival probability held as a dependent variable.

12. (Currently amended) The method of claim 2, ~~wherein correlating comprises~~ further comprising:

determining whether [[the]] said normalized expression values of said first plurality of genes is similar to said normalized reference expression values obtained for said second plurality of genes ~~from DLBCL patients~~ stratified into said classification groups selected from [[having]] low, medium [[or]] and high overall survival probability after anthracycline-based chemotherapy.

13 – 39. (Cancelled)

40. (Currently amended) A kit comprising assays for measuring expression of a first plurality of genes in a tumor sample from a patient having DLBCL, wherein normalized expression values of said first plurality of genes are correlated to normalized reference values of ~~[[the]]~~ a second plurality of genes in tumor samples from a plurality of DLBCL patients stratifies ~~[[the]]~~ said plurality of DLBCL patients into at least one of a plurality of classification groups, the kit comprising:

a plurality of primers designed to hybridize to the first plurality of genes in the tumor sample from a patient having DLBCL;

a database comprising the normalized reference values of the second plurality of genes; and

an algorithm for determining which of the at least one of a plurality of classification groups includes the patient having DLBCL.

41. (Currently amended) The kit of claim 40, wherein ~~[[the]]~~ said normalized reference expression of said second plurality of genes classify said plurality of DLBCL patients ~~in~~ into at least one of a plurality of classification groups that is predictive of a probability of survival.

42. (Currently amended) The kit of claim 41 wherein said probability of survival comprises a probability of survival after anthracycline-based chemotherapy.

43. (Currently amended) The kit of claim 40, wherein ~~[[the]]~~ said PCR assays are real-time RT-PCR assays.

44. (Currently amended) The kit of claim 40, ~~which further comprises~~ comprising:
an assay for measuring expression of a housekeeping gene in ~~[[a]]~~ said tumor sample, wherein said normalized expression values of said first plurality of genes comprise ratios of ~~gene~~ measured expression values of said first plurality of genes to measured expression values of ~~[[the]]~~ said housekeeping gene.

45. (Previously presented) The kit of claim 44, wherein the housekeeping gene is *PGK1* or *GAPDH*.

46. (Previously presented) The kit of claim 45, wherein the housekeeping gene is *PGK1*.

47. (Currently amended) The kit of claim 41 wherein ~~the survival probability~~ said classification groups comprise the groups of low, medium, ~~[[or]]~~ and high ~~overall~~ probability of survival after anthracycline-based chemotherapy.

48. (Currently amended) The kit of claim ~~[[46]]~~ 41, wherein ~~the survival probability~~ said classification groups ~~further~~ comprise~~[[s]]~~ the groups of low, medium ~~[[or]]~~ and high International Prognostic Index score.

49. (Currently amended) The kit of claim 40, wherein ~~[[the]]~~ said first plurality of genes comprise at least ~~two~~ four genes selected from the group consisting of *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3* and *BCL-2*.

50. (Currently amended) The kit of claim 49, wherein one of ~~[[the]]~~ said at least ~~two~~ four genes is *BCL-6*.

51. (Currently amended) The kit of claim 41, wherein ~~[[the]]~~ said first plurality of genes comprise *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3* and *BCL-2*.

52. (Currently amended) The kit of claim 51, wherein ~~[[the]]~~ said second plurality of genes consists of *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3* and *BCL-2*.

53. (Currently amended) ~~The kit of claim 52,~~ A kit comprising:
assays for measuring expression of a plurality of genes in a tumor sample from a
patient having DLBCL;
wherein normalized expression of the plurality of genes in tumor samples from
DLBCL patients stratifies the patients into classification groups, wherein the plurality of genes
classify DLBCL patients in groups predictive of probability of survival;
wherein the plurality of genes consists of *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3*
and *BCL-2*;
wherein survival probability is based upon weighed predictor Z in formula:
$$Z = (A \times LMO2) + (B \times BCL6) + (C \times FN1) + (D \times CCND2) + (E \times SCYA3) + (F \times BCL2)$$

wherein A is about -0.03, B is about -0.2, C is about -0.2, D is about 0.03, E is about 0.2 and F is about 0.6 and wherein LMO2, BCL6, FN1, CCND2, SCYA3 and BCL2 are log base 2 of normalized expression values for genes *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3* and *BCL-2*, respectively.

54. (Original) The kit of claim 52 wherein A is about - 0.0273, B is about -0.2103, C is about -0.1878, D is about 0.0346, E is about 0.1888, and F is about 0.5527.

55. (Original) The kit of claim 53, wherein a Z value of less than about -0.06 indicates high probability of survival, a Z value of from about -0.06 to about 0.09 indicates medium probability of survival and a Z value of greater than about 0.09 indicates low probability of survival.

56. (Original) The kit of claim 55, wherein a Z value of less than about -0.063 indicates high probability of survival, a Z value of from about -0.063 to about 0.093 indicates medium probability of survival and a Z value of greater than about 0.093 indicates low probability of survival.

57 - 76. (Cancelled)

77. (New) The method of Claim 1 further comprising stratifying said classification groups into at least the groups of low, medium, and high overall survival probability.

78. (New) A kit for determining a survival probability of a patient diagnosed with DLBCL, the kit comprising:

a plurality of primers designed to measure expression of a first plurality of predictive genes in a tumor sample;

a database comprising expression data from a second plurality of predictive genes obtained from DLBCL patients with known survival data; and

an algorithm for correlating a normalized expression of said first plurality of predictive genes in a tumor sample to said expression data from a second plurality of predictive genes.

79. (New) The kit of Claim 78 further comprising a housekeeping gene operable in normalizing a measured expression of said first plurality of predictive genes.

80. (New) The kit of Claim 78 further comprising expression data collected from a reference cell line.

81. (New) The kit of Claim 78 further comprising a plurality of classification groups stratified from said expression data from a second plurality of predictive genes.

82. (New) The kit of Claim 81 further comprising a second algorithm for classifying normalized expression data from said first plurality of predictive genes into at least one of said plurality of classification groups.

83. (New) The kit of Claim 78 wherein at least one of said first plurality of predictive genes is selected from the group consisting of *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3* and *BCL-2*.

84. (New) The kit of Claim 78, wherein at least one of said second plurality of predictive genes is selected from the group consisting of *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3* and *BCL-2*.

85. (New) The kit of Claim 78 further comprising a naturally occurring or recombinant reverse transcriptase enzyme.

86. (New) A method for determining a survival probability of a patient diagnosed with DLBCL, the method comprising:

amplifying a first plurality of genes;

measuring expression for said first plurality of genes;

normalizing expression for said first plurality of genes to produce normalized expression values; and

correlating said normalized expression values of said first plurality of genes to data stratified into classification groups to determine the probability of survival of the patient diagnosed with DLBCL.

87. (New) The method of Claim 86 further comprising performing reverse transcriptase on mRNA from the patient.

88. (New) The method of Claim 86 wherein said data stratified in classification groups comprises normalized expression values of a second plurality of genes collected from DLBCL patients with a known survival.

89. (New) The method of Claim 86 wherein at least one of said first plurality of genes is selected from the group consisting of *LMO2*, *BCL-6*, *FN1*, *CCND2*, *SCYA3* and *BCL-2*.

90. (New) The method of Claim 86 further comprising providing a plurality of primers designed to hybridize to said first plurality of genes.

91. (New) The method of Claim 86 further comprising performing Real-Time PCR on said first plurality of genes.

92. (New) The method of Claim 86 further comprising preamplifying said first plurality of genes.